

GenCore version 5.1.6
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OM protein - nucleic search, using frame p2n.p2n model

Run on: January 15, 2006, 21:47:59 ; Search time 42759 Seconds
(without alignments)
1261.593 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSSGLMSQKVTSPYWEERI.....RLLCDAYMCYQSPMTSLYK 949

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 18

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%

Maximum Match 100%

Listing first 500 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-O=/cgn2_1/USPTO_spool_p/US09671687/runat_13012006_114913_2460/app_query.fasta_1.1095
-DB=GenBank -QFMT=fastap -SUFFIX=90pct.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=500
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=90 -ALIGN=500 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09671687@cgn 1.1 5931 @runat_13012006_114913_2460 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenBank 149: *
1: gb_ha.*
2: gb_in.*
3: gb_env.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_hgt.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4983	99.0	3302	6	CQ834224 Sequence
2	4983	99.0	3540	8	BC012342 Homo sapi
3	4983	99.0	5414	6	CS034166 Sequence

RESULT 1

CQ834224

LOCUS

DEFINITION

SEQUENCE 95 from Patent WO2004058805.

ACCESSION

CQ834224

VERSION

CQ834224.1

KEYWORDS

GI:50833761

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1

AUTHORS

Matsuda A. and Yoneta, S.

T cell activating gene

TITLE

Patent: WO 2004058805-A 95 15-JUL-2004;

Asahi Kasei Pharma Corporation (JP)

JOURNAL

FEATURES

Location/Qualifiers

source

1..3302

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

243..3104

/notes="unnamed protein product"

/codon_start=1

/protein_id="CAH05327.1"

/db_xref="GI:50833762"

/translation="MSSGLMSQKVTSPYWEERI FYLLQECSTVDKQTKLKVPGK

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ORIGIN

Alignment Scores:

Pred. No.: 0

Score: 4983.00

Length: 3302

Matches: 948

Percent Similarity: 99.48%

Conservative: 0

Best Local Similarity: 99.48%

Mismatches: 1

Indels: 4

Query Match: 98.99%

Gaps: 4

ALIGNMENTS

CQ834224

Sequence 95 from Patent WO2004058805.

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CQ834224

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/protein_id="CAH05327.1"

/db_xref="GI:50833762"

/translation="MSSGLMSQKVTSPYWEERI FYLLQECSTVDKQTKLKVPGK

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